

pable of binding to a region in the SRCR domains I-II of the CD163 receptor, or a variant thereof.

5 It is preferred that the Hp-Hb complex or a part thereof or a mimic thereof is available in a purified and/or isolated form.

According to the invention the term "Hp-Hb complex" is meant to include functional equivalents of the Hp-Hb complex comprising a predetermined amino acid sequence. In the present context the term "predetermined amino acid sequence of Hp-Hb complex" relates to both  
10 the haptoglobin sequence and the haemoglobin sequence.

The predetermined sequence of a haptoglobin chain may be any of the sequences shown in Fig. 4a and 4b, i.e. any of the sequences having the sequence identification in the sequence database SWISS-PROT (sp) or trEMBL (tr).

15 sp|P00737|HPT1\_HUMAN  
sp|P00738|HPT2\_HUMAN  
sp|P50417|HPT\_ATEGE  
tr|Q60574|Q60574  
20 tr|Q61646|Q61646  
sp|Q62558|HPT\_MUSSA  
sp|P06866|HPT\_RAT  
tr|O35086|O35086  
sp|P19006|HPT\_CANFA

25 A predetermined amino acid sequence for a haemoglobin chain may be any of the sequences mentioned below together with accession No. in the sequence database SWISS-PROT:

30 sp|P01922|HBA\_HUMAN HEMOGLOBIN ALPHA CHAIN –  
Homo sapiens (Human), Pan troglodytes (Chimpanzee), and Pan paniscus (Pygmy chimpanzee) (Bonobo).

35 VLSPADKTNVKAAGKVGGAHAGEYGAEALERMFSLFPTTKTYFPHFDLSH  
GSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLRVDPVNFKL  
LSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR

sp|P02023|HBB\_HUMAN HEMOGLOBIN BETA CHAIN –

Homo sapiens (Human), Pan troglodytes (Chimpanzee), and Pan paniscus (Pygmy chimpanzee) (Bonobo).

5 VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLST  
PDAVMGNPKVKAHGKKVLGAFSDGLAHLNLTGTFATLSELHCDKLHVD  
ENFRLLGNLVLCVLAHFGKEFTPPVQAAYQKVVAGVANALAHKYH

sp|P02042|HBD\_HUMAN HEMOGLOBIN DELTA CHAIN –  
Homo sapiens (Human).

10 VHLTPEEKTAVALWGKVNVDAVGGEALGRLLVVYPWTQRFFESFGDLSS  
PDAVMGNPKVKAHGKKVLGAFSDGLAHLNLTGTFSLSELHCDKLHVD  
ENFRLLGNLVLCVLARNFGKEFTPQMQAAYQKVVAGVANALAHKYH

15 sp|P02096|HBG\_HUMAN HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS - Homo  
sapiens (Human), and Pan troglodytes (Chimpanzee).

20 GHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSS  
ASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVD  
ENFKLLGNLVTVLAIHFGKEFTPEVQASWQKMTAVASALSSRYH

sp|P09105|HBAT\_HUMAN HEMOGLOBIN THETA-1 CHAIN –  
Homo sapiens (Human).

25 ALSAEDRALVRALWKKLGSNVGYTTEALERTFLAFPATKTYFSHLDLSP  
GSSQVRAHGQKVADALSLAVERLDDLPHALSALSHLHACQLRVPDPAFQL  
LGHCLLVTLARHYPGDFSPALQASLDKFLSHVISALVSEYR

30 sp|P02008|HBAZ\_HUMAN HEMOGLOBIN ZETA CHAIN –  
Homo sapiens (Human).

LSLTKTERTIIVSMWAKISTQADTIGTETLERFLSHPQTKTYFPHFDLHP  
GSAQLRAHGSKVVAVGDAVKSIDDIGGALSKLSELHAYILRVPVNFKL  
LSHCLLVTLAARFPADFTAEAHAAWDKFLSVSVSLTEKYR

sp|P02100|HBE\_HUMAN HEMOGLOBIN EPSILON CHAIN –  
Homo sapiens (Human).

VHFTAEEKAAVTSLSKMNVEEAGGEALGRLLVYPWTQRFFDSFGNLSS  
 PSAILGNPKVKAHGKKVLTSGDAIKNMDNLKPAFAKSELHCDKLHVDP  
 ENFKLLGNVMVILATHFGKEFTPEVQAAWQKLVSVAVALAHKYH

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tr[Q14510]Q14510 SICKLE BETA-HEMOGLOBIN MRNA –  
 Homo sapiens (Human).

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MVHLTPVEKSAVTAXWGKVNDEVGGEALGRLLVYPWTRFFESFGDLS  
 TPDVVMGNPKVKAHGKKVLGAFSDGLAHLNLDLKGTFATLSELHCDKLHVD  
 PENFRLLGNVLVCVLAHHFGKEFTPPVQAAVQKVVAGVANALAHKYH

A "functional equivalent" is defined as:

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i) equivalents comprising an amino acid sequence capable of being recognised by an antibody also capable of recognising the predetermined amino acid sequence, and/or

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ii) equivalents comprising an amino acid sequence capable of binding to a receptor moiety also capable of binding the predetermined amino acid sequence, and/or

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iii) equivalents having at least a substantially similar or higher binding affinity to CD163 as at least a monomeric Hp-Hb complex comprising said predetermined amino acid sequence.

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According to the present invention a functional equivalent of a Hp-Hb complex or fragments thereof may be obtained by addition, substitution or deletion of at least one amino acid in either or both of the haptoglobin sequence and the haemoglobin sequence. Thus, a functional equivalent of the Hp-Hb complex may comprise a modification of either of the components of the complex or both.

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When the amino acid sequence comprises a substitution of one amino acid for another, such a substitution may be a conservative amino acid substitution. Fragments of the complex according to the present invention may comprise more than one such substitution, such as e.g. two conservative amino acid substitutions, for example three or four conservative amino acid substitutions, such as five or six conservative amino acid substitutions, for example seven or eight conservative amino acid substitutions, such as from 10 to 15 conservative amino acid substitutions, for example from 15 to 25 conservative amino acid substitution. Substitutions can be made within any one or more groups of predetermined amino acids.